

ZIP: 54010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,003

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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2016 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..2013
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-758-003-1

Query Match      7.5%; Score 14; DB 1; Length 2016;
Best Local Similarity 60.5%; Pred. No. 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 CTCAAAGTCTCAGACACCAAGATCGACGATCGAGGA 536
   ||||| ||| ||| ||| ||| ||| ||| |||
Db 87 CCCAAGGCTCCGCTGTCAGTTCTGCACTCTCCAGGA 50

```

Search completed: February 9, 2005, 08:45:53
Job time : 0.001 secs

;; CITY: HILLSBOROUGH
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94010
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/758,003
;; FILING DATE: 09-Jan-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/132,118
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OSMAN, RICHARD A.
;; REGISTRATION NUMBER: 36,627
;; REFERENCE/DOCKET NUMBER: T95-006-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 343-4341
;; TELEFAX: (650) 343-4342
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 671 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-758-003-2

Alignment Scores:
Pred. No.: 0 Length: 671
Score: 47.00 Matches: 42
Percent Similarity: 34.86% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 76
Query Match: 1.53% Indels: 39
DB: 1 Gaps: 11

US-09-824-134-1 (1-1701) x US-09-758-003-2 (1-671)

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Qy 1455 CTC AATTCGTCCTGG---CAACCATCACTG-----CCC 1426
Db 354 ValGluGluSerTrpPheAlaProSerLeuGluHisProGlnGluAsnGluProSer 373
Qy 1425 CTACTTAGCAGTCTCAGAGGAGGACTCACTC---ACACAGGGGGCAAGAGCTGGACCA 1369
Db 374 LeuGlnSerLysLeuGlnAspGluAlaAsnTyrHisLeuTyrGlySerArgMetAspArg 393
Qy 1368 CGGCCAACACAGGTCTCCCCACCCGCCAGCCAT-----GCCTCTCCCCACCAC 1318
Db 394 GlnThrLysGlnGlnProArgGlnAsnValAlaTyrAsnArgGluGluArgArgArg 413
Qy 1317 AGCACCCCGCTGACCTAGTGTCCAGGTCTGTCCC-----GGTGGCCTCCAA 1270
Db 414 ArgValSerHisAspPheAlaGlnGlnArgProTyrGluAsnPheGlnAsnThrGlu 433
Qy 1269 GGAATGGGACAAACATCTTCTGCGCACTGCAGGG---GCACGACAGCCGACAGT 1213
Db 434 GlyLysGlyThrValTyrSerSerAlaAlaSerHisGlyAsnAlaValHisGlnProSer 453
Qy 1212 GGTGTAGCA-----TGGGCTCTGGTGAAGGATGGGGG----- 1180
Db 454 GlyLeuThrSerGlnProGlnValLeuTyrGlnAsnAsnGlyLeuTyrSerSerHisGly 473
Qy 1179 ---GGTTCAATCCAGTCTCCACCTCTCTGCTGTGCTCCGATTCCTGGCCCTCTGAGC 1123
Db 474 PheGlyThrArgProLeuAspProGlyThrAla-----GlyProArgVal 488
Qy 1122 TGGTCTCTCCGCTGGGAGTAACAGTGTGACTGTCTCATCT---GCACAGATTCTCT----- 1070
Db 489 TrpTyrArgProIleProSerHisMetProSerLeuHisAsnIleProValProGluThr 508
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Qy 1069 TCTGTGCTGGACACGGTTCCAACT-----TTCCAACTACTCCCG 1031
Db 509 AsnTyrLeuGlyAsnThrProThrMetProPheSerSerLeuPro 523

Search completed: February 9, 2005, 08:56:37
Job time: 1 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: February 9, 2005, 09:04:15 ; Search time 0.001 Seconds
(without alignments)
1032.192 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 1302
Sequence: 1 VNQAPECFGGILGLPKR.....RSGAMSPMNSDASTSEAS 256

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1 seqs, 2016 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=soft -Q=US09824134.p2n -DB=US09758003.seq
-SUFFIX=ptc -OUT=US09824134-2.p2n.align -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6
-NO_XLPHY -NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: US09758003.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111.5	8.6	2016	1	US-09-758-003-1
2	48	3.7	2016	1	US-09-758-003-1

ALIGNMENTS

RESULT 1
US-09-758-003-1
Sequence 1, Application US/09758003
GENERAL INFORMATION:
APPLICANT: BAICHUWAL, VIJAY R
HUANG, JIANING
HSU, HAILING
GOEDDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE

CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/758,003
FILING DATE: 09-Jan-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/132,118
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2013
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-758-003-1

Alignment Scores:
Pred. No.: 0
Score: 111.50
Percent Similarity: 61.04%
Best Local Similarity: 36.36%
Query Match: 8.56%
DB: 1

Length: 2016
Matches: 28
Conservative: 19
Mismatches: 27
Indels: 3
Gaps: 3

US-09-824-134-2 (1-256) x US-09-758-003-1 (1-2016)
QY 152 IleCysAspAsnValGlyAspTrpArgLeuAlaArgGlnLeuLysValSerAsp 171
DB 1768 ATCAGGAAATCTGGAAAGCACCTGGAAAACTGTCCCGTAACTGGGCTTCACACAG 1827

QY 172 ThrLysIleAspSerIleGluAspArgTyrProArgAsn---LeuThrGluArgValArg 190
DB 1828 TCTCAGATTGATGAATTCACCATGACATATGACGCGATGGACTGAAAGAAAAGTTTAC 1887
QY 191 GluSerLeuArgIleTrpLysAsnThrGluLys---GluAsnAlaThrValAlaHisLeu 209
DB 1888 CAGATGCTCCAAAAGTGGGTGATGAGGAAAGGCATAAAGGGAGCCACCGTGGGGAAGCTG 1947

QY 210 ValGlyAlaLeuArgSerCys---GlnMetAsnLeuValAlaAspLeuVal 225
DB 1948 GCCCAGGGCGCTCCACAGGTTCAGGATCGACCTTCTGAGCAGCTTGATT 1998

RESULT 2
US-09-758-003-1/c
Sequence 1, Application US/09758003
GENERAL INFORMATION:
APPLICANT: BAICHUWAL, VIJAY R
HUANG, JIANING
HSU, HAILING
GOEDDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 09:01:06 ; Search time 0.001 Seconds
(without alignments)
77.836 Million cell updates/sec

Title: US-09-824-134-2
Perfect score: 593
Sequence: 1 FEAGAAGAAGBEDLCAAF.....QEVOQARDLQNRSGAMSPMS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 671 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : US09758003.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111.5	18.8	671	1 US-09-758-003-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-758-003-2
Sequence 2, Application US/09758003
GENERAL INFORMATION:
APPLICANT: BAICHWAL, VIJAY R
HUANG, JIANING
HSU, HAILING
GOEDDEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING ASSAYS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
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FILING DATE: 09-Jan-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T95-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 671 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-758-003-2

Query Match 18.8%; Score 111.5; DB 1; Length 671;
Best/Local Similarity 36.4%; Pred. No. 0;
Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;
Qy 152 ICDNVGKDWRLARQLKVSPTKIDSIEDRYPRN-LTERVRESLRIWKTEK-ENATVAHL 209
Db 590 IRENLGKHWKNCARKLGFTQSOIDEIDHDYERDGLKEKVKYQMLQKVMREGIKGATVGKL 649
Qy 210 VGALRSC-QMNLVADLV 225
Db 650 AQALHQC-SRIDLLSLI 666

Search completed: February 9, 2005, 09:01:07
Job time : 1 secs

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